



1

#7

SEQUENCE LISTING

<110> Ota, Toshio  
Isogai, Takao  
Nishikawa, Tetsuo  
Hayashi, Koji  
Otsuka, Kaoru  
Yamamoto, Jun-ichi  
Ishii, Shizuko  
Sugiyama, Tomoyasu  
Wakamatsu, Ai  
Nagai, Keiichi  
Otsuki, Tetsuji  
Funahashi, Shin-ichi  
Miyata, Shoji

<120> NOVEL GENES ASSOCIATED WITH THE  
MAINTENANCE OF DIFFERENTIATION OF SMOOTH MUSCLE CELLS

<130> 06501-097001

<140> US 10/058,518

<141> 2002-01-28

<150> PCT/JP00/05059

<151> 2000-07-28

<150> US 60/183,322

<151> 2000-02-17

<150> US 60/159,590

<151> 1999-10-18

<150> JP 11-248036

<151> 1999-07-29

<150> JP 2000-118776

<151> 2000-01-11

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 agcc atg gca gcg ctg cgc tac gcg ggg ctg gac gac acg gac agt gag 169  
 Met Ala Ala Leu Arg Tyr Ala Gly Leu Asp Asp Thr Asp Ser Glu  
 1 5 10 15  
  
 gac gag ctg cct ccg ggc tgg gag gag aga acc acc aag gac ggc tgg 217  
 Asp Glu Leu Pro Pro Gly Trp Glu Glu Arg Thr Thr Lys Asp Gly Trp  
 20 25 30  
  
 gtt tac tac gcc aat cac acc gag gag aag act cag tgg gaa cat cca 265  
 Val Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro  
 35 40 45  
  
 aaa act gga aaa aga aaa cga gtg gca gga gat ttg cca tac gga tgg 313  
 Lys Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp  
 50 55 60  
  
 gaa caa gaa act gat gag aac gga caa gtg ttt ttt gtt gac cat ata 361  
 Glu Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile  
 65 70 75  
  
 A1 aat aaa aga acc acc tac ttg gac cca aga ctg gcg ttt act gtg gat 409  
 Asn Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp  
 80 85 90 95  
  
 gat aat ccg acc aag cca acc acc cgg caa aga tac gac ggc agc acc 457  
 Asp Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr  
 100 105 110  
  
 act gcc atg gaa att ctc cag ggc ccg gat ttc act ggc aaa gtg gtt 505  
 Thr Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val  
 115 120 125  
  
 gtg gtc act gga gct aat tca gga ata ggg ttc gaa acc gcc aag tct 553  
 Val Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser  
 130 135 140  
  
 ttt gcc ctc cat ggt gca cat gtg atc ttg gcc tgc agg aac atg gca 601  
 Phe Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala  
 145 150 155  
  
 agg gcg agt gaa gca gtg tca cgc att tta gaa gaa tgg cat aaa gcc 649  
 Arg Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala  
 160 165 170 175  
  
 aag gta gaa gca atg acc ctg gac ctc gct ctg ctc cgt agc gtg cag 697  
 Lys Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln  
 180 185 190  
  
 cat ttt gct gaa gca ttc aag gcc aag aat gtg cct ctt cat gtg ctt 745  
 His Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu  
 195 200 205  
  
 gtg tgc aac gca gca act ttt gct cta ccc tgg agt ctc acc aaa gat 793  
 Val Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp  
 210 215 220

ggc ctg gag acc acc ttt caa gtg aat cat ctg ggg cac ttc tac ctt 841  
 Gly Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu  
 225 230 235  
 gtc cag ctc ctc cag gat gtt ttg tgc cgc tca gct cct gcc cgt gtc 889  
 Val Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val  
 240 245 250 255  
 att gtg gtc tcc tca gag tcc cat cga ttt aca gat att aac gac tcc 937  
 Ile Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser  
 260 265 270  
 ttg gga aaa ctg gac ttc agt cgc ctc tct cca aca aaa aac gac tat 985  
 Leu Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr  
 275 280 285  
 tgg gcg atg ctg gct tat aac agg tcc aag ctc tgc aac atc ctc ttc 1033  
 Trp Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe  
 290 295 300  
 tcc aac gag ctg cac cgt cgc ctc tcc cca cgc ggg gtc acg tcg aac 1081  
 Ser Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn  
 305 310 315  
 gca gtg cat cct gga aat atg atg tac tcc aac att cat cgc agc tgg 1129  
 Ala Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp  
 320 325 330 335  
 tgg gtg tac aca ctg ctg ttt acc ttg gcg agg cct ttc acc aag tcc 1177  
 Trp Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser  
 340 345 350  
 atg caa cag gga gct gcc acc acc gtg tac tgt gct gct gtc cca gaa 1225  
 Met Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu  
 355 360 365  
 ctg gag ggt ctg gga ggg atg tac ttc aac aac tgc tgc cgc tgc atg 1273  
 Leu Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met  
 370 375 380  
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 Pro Ser Pro Glu Ala Gln Ser Glu Glu Thr Ala Arg Thr Leu Trp Ala  
 385 390 395  
 ctc agc gag agg ctg atc caa gaa cgg ctt ggc agc cag tcc ggc 1366  
 Leu Ser Glu Arg Leu Ile Gln Glu Arg Leu Gly Ser Gln Ser Gly  
 400 405 410  
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A1

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gtacttgtca tagactcctt tgctaattgct atgcaaaaaa ttcttttagag attataacaa 2026
atTTTTcaaa tcattcctta gataccttga aaggcaggaa gggaagcgta tataacttaag 2086
aatacacagg atatTTTTggg gggcagagaa taaaacgtta gttaatccct ttgtctgtca 2146
atcacagtct cagttctctt gctttcacat tgtacttaaa cctcctgctg tgcctcgcat 2206
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20 25 30  
Tyr Tyr Ala Asn His Thr Glu Glu Lys Thr Gln Trp Glu His Pro Lys  
35 40 45  
Thr Gly Lys Arg Lys Arg Val Ala Gly Asp Leu Pro Tyr Gly Trp Glu  
50 55 60  
Gln Glu Thr Asp Glu Asn Gly Gln Val Phe Phe Val Asp His Ile Asn  
65 70 75 80  
Lys Arg Thr Thr Tyr Leu Asp Pro Arg Leu Ala Phe Thr Val Asp Asp  
85 90 95  
Asn Pro Thr Lys Pro Thr Thr Arg Gln Arg Tyr Asp Gly Ser Thr Thr  
100 105 110  
Ala Met Glu Ile Leu Gln Gly Pro Asp Phe Thr Gly Lys Val Val Val  
115 120 125  
Val Thr Gly Ala Asn Ser Gly Ile Gly Phe Glu Thr Ala Lys Ser Phe  
130 135 140  
Ala Leu His Gly Ala His Val Ile Leu Ala Cys Arg Asn Met Ala Arg  
145 150 155 160  
Ala Ser Glu Ala Val Ser Arg Ile Leu Glu Glu Trp His Lys Ala Lys  
165 170 175  
Val Glu Ala Met Thr Leu Asp Leu Ala Leu Leu Arg Ser Val Gln His  
180 185 190  
Phe Ala Glu Ala Phe Lys Ala Lys Asn Val Pro Leu His Val Leu Val  
195 200 205  
Cys Asn Ala Ala Thr Phe Ala Leu Pro Trp Ser Leu Thr Lys Asp Gly  
210 215 220  
Leu Glu Thr Thr Phe Gln Val Asn His Leu Gly His Phe Tyr Leu Val  
225 230 235 240  
Gln Leu Leu Gln Asp Val Leu Cys Arg Ser Ala Pro Ala Arg Val Ile  
245 250 255  
Val Val Ser Ser Glu Ser His Arg Phe Thr Asp Ile Asn Asp Ser Leu  
260 265 270  
Gly Lys Leu Asp Phe Ser Arg Leu Ser Pro Thr Lys Asn Asp Tyr Trp  
275 280 285  
Ala Met Leu Ala Tyr Asn Arg Ser Lys Leu Cys Asn Ile Leu Phe Ser  
290 295 300  
Asn Glu Leu His Arg Arg Leu Ser Pro Arg Gly Val Thr Ser Asn Ala  
305 310 315 320  
Val His Pro Gly Asn Met Met Tyr Ser Asn Ile His Arg Ser Trp Trp  
325 330 335  
Val Tyr Thr Leu Leu Phe Thr Leu Ala Arg Pro Phe Thr Lys Ser Met

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Gln Gln Gly Ala Ala Thr Thr Val Tyr Cys Ala Ala Val Pro Glu Leu
      355      360      365
Glu Gly Leu Gly Gly Met Tyr Phe Asn Asn Cys Cys Arg Cys Met Pro
      370      375      380
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gaa gaa aaa aca cag tgg gaa cat cca aaa tct ggg aag agg aaa cgt      95
Glu Glu Lys Thr Gln Trp Glu His Pro Lys Ser Gly Lys Arg Lys Arg
          20          25          30

gtt gca gga ggt ctg cca tat gga tgg gag cag gag act gat gaa aat      143
Val Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn
          35          40          45

gga cag gtc tat ttt gta gac cac ata aac aaa aga act acc tat ctg      191
Gly Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu
          50          55          60

gat cca aga ttg gcc ttt aca gtt gaa gat aat cca gca aag cca cct      239
Asp Pro Arg Leu Ala Phe Thr Val Glu Asp Asn Pro Ala Lys Pro Pro
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act aga caa aaa      251
Thr Arg Gln Lys
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<210> 4  
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 <213> Gallus gallus

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          20          25          30
Ala Gly Gly Leu Pro Tyr Gly Trp Glu Gln Glu Thr Asp Glu Asn Gly
          35          40          45

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Gln Val Tyr Phe Val Asp His Ile Asn Lys Arg Thr Thr Tyr Leu Asp  
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 Arg Gln Lys

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<210> 7  
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<220>  
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<400> 7  
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<210> 8  
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A1

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